

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2270	94.7	1563	32 US-09-857-581-35	Sequence 35, Appl
2	2270	94.7	1563	58 US-60-144-783-35	Sequence 1, Appl1
3	2269	94.7	1756	1 PCT-US02-11260-1	Sequence 1, Appl1
4	2269	94.7	1756	32 US-09-857-581-1	Sequence 1, Appl1
5	2269	94.7	1756	40 US-10-104-706-1	Sequence 1, Appl1
6	2269	94.7	1756	40 US-10-104-706A-1	Sequence 1, Appl1
7	2269	94.7	1756	41 US-10-171-174A-9	Sequence 1, Appl1
8	2269	94.7	1756	55 US-60-117-769-1	Sequence 1, Appl1
9	2269	94.7	1756	58 US-60-144-783-1	Sequence 1, Appl1
10	2269	94.7	1756	75 US-60-311-461-1	Sequence 1, Appl1
11	2268	94.7	1566	32 US-09-857-581-23	Sequence 23, Appl
12	2268	94.7	1566	32 US-09-857-581-25	Sequence 25, Appl
13	2268	94.7	1566	32 US-09-857-581-27	Sequence 27, Appl
14	2268	94.7	1566	32 US-09-857-581-31	Sequence 31, Appl
15	2268	94.7	1566	32 US-09-857-581-33	Sequence 33, Appl
16	2268	94.7	1566	58 US-60-144-783-23	Sequence 23, Appl
17	2268	94.7	1566	58 US-60-144-783-25	Sequence 25, Appl
18	2268	94.7	1566	58 US-60-144-783-27	Sequence 27, Appl
19	2268	94.7	1566	58 US-60-144-783-31	Sequence 31, Appl
20	2268	94.7	1566	58 US-60-144-783-33	Sequence 33, Appl
21	2267	94.6	1566	32 US-09-857-581-29	Sequence 29, Appl
22	2267	94.6	1566	58 US-60-144-783-29	Sequence 29, Appl
23	2267	94.6	1694	42 US-10-219-999-3561	Sequence 367, Ap
24	2267	94.6	1709	77 US-60-337-358-367	Sequence 1, Appl1
25	2267	94.6	1717	35 US-09-936-190-1	Sequence 1216, Ap
26	2267	94.6	1884	25 US-09-654-617-1216	

65: /cgn2\_6/prodata/1/pna/US6021\_COMB.seq:\*  
66: /cgn2\_6/prodata/1/pna/US6022\_COMB.seq:\*  
67: /cgn2\_6/prodata/1/pna/US6023\_COMB.seq:\*  
68: /cgn2\_6/prodata/1/pna/US6024\_COMB.seq:\*  
69: /cgn2\_6/prodata/1/pna/US6025\_COMB.seq:\*  
70: /cgn2\_6/prodata/1/pna/US6026\_COMB.seq:\*  
71: /cgn2\_6/prodata/1/pna/US6027\_COMB.seq:\*  
72: /cgn2\_6/prodata/1/pna/US6028\_COMB.seq:\*  
73: /cgn2\_6/prodata/1/pna/US6029\_COMB.seq:\*  
74: /cgn2\_6/prodata/1/pna/US6030\_COMB.seq:\*  
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82: /cgn2\_6/prodata/1/pna/US6038\_COMB.seq:\*  
83: /cgn2\_6/prodata/1/pna/US6039\_COMB.seq:\*  
84: /cgn2\_6/prodata/1/pna/US6040\_COMB.seq:\*  
85: /cgn2\_6/prodata/1/pna/US6041\_COMB.seq:\*

#### ALIGNMENTS

27	2267	94.6	1884	27 US-09-684-016-1216	Sequence 1216, Ap
28	2251	93.9	1824	18 US-09-453-315-13	Sequence 13, Appl
29	2251	93.9	1824	32 US-09-857-581-9	Sequence 9, Appl1
30	2251	93.9	1824	58 US-60-144-783-9	Sequence 9, Appl1
31	2201.5	91.9	1900	32 US-09-857-581-53	Sequence 53, Appl
32	2201.5	91.9	1900	58 US-60-144-783-53	Sequence 53, Appl
33	2193	91.5	1801	32 US-09-857-581-52	Sequence 52, Appl
34	2193	91.5	1801	58 US-60-144-783-52	Sequence 52, Appl
35	2186	91.2	2059	25 US-09-654-617-1217	Sequence 1217, Ap
36	2186	91.2	2059	27 US-09-684-016-1217	Sequence 1217, Ap
37	2183	91.1	1501	32 US-09-857-581-56	Sequence 56, Appl
38	2180	91.0	1501	32 US-09-857-581-15	Sequence 15, Appl
39	2180	91.0	1501	58 US-60-144-783-15	Sequence 15, Appl
40	2179	90.9	1501	32 US-09-857-581-39	Sequence 39, Appl
41	2179	90.9	1501	58 US-60-144-783-39	Sequence 39, Appl
42	2178	90.9	1501	32 US-09-857-581-19	Sequence 19, Appl
43	2178	90.9	1501	32 US-09-857-581-58	Sequence 58, Appl
44	2178	90.9	1501	58 US-60-144-783-19	Sequence 19, Appl
45	2177	90.9	1501	32 US-09-857-581-21	Sequence 21, Appl

RESULT 1  
US-09-857-581-35  
: Sequence 35, Application US/09857581

: GENERAL INFORMATION:  
: APPLICANT: E. I. du Pont de Nemours and Company  
: TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase  
: FILE REFERENCE: B81339 PCT  
: CURRENT APPLICATION NUMBER: US/09/857,581  
: PRIOR FILING DATE: 2001-06-05  
: PRIOR APPLICATION NUMBER: 60/117,769  
: PRIOR FILING DATE: 1999-01-27  
: PRIOR APPLICATION NUMBER: 60/144,783  
: PRIOR FILING DATE: 1999-07-20  
: PRIOR APPLICATION NUMBER: 60/156,094  
: PRIOR FILING DATE: 1999-09-24  
: NUMBER OF SEQ ID NOS: 66  
: SOFTWARE: Microsoft Office 97  
: SEQ ID NO 35  
: LENGTH: 1563  
: TYPE: DNA  
: ORGANISM: Pisum sativum

US-09-857-581-35  
Alignment Scores:

Pred. No.: 9,896-260 Length: 1563  
Score: 2270.00 Matches: 454  
Percent Similarity: 87.14% Conservative: 0  
Best Local Similarity: 87.14% Mismatches: 67  
Query Match: 94.74% Indels: 0  
DB: 32 Gaps: 0

US-09-857-581-66 (1-521) x US-09-857-581-35 (1-1563)

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Db      841  GAGGACGAGCATGAGATCAAAATTACCAAGGCAATCAAGGCGCTTGTTCGAC  900
Qy      301  ***PheSerAlaIy***AspSerThrAla*****ThrIuIupAlaLeuAlaGluLeu  320
Db      901  TTTTCTCTCGAGGAGCAAGATTCCACAGCGGTGGCAACAGAGTGGCAATTGGCAGAGCTC  960
Qy      321  ILeaenAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValAlaGlyLys  340
Db      961  ATCAACAAATCCCAAGSGTGTTCGAAAAGCGTCTGTGAGAGAGGTCTACAGTGTTCGGCAAA  1020
Qy      341  Asp***LeuValAspGluValAspThrGlnaenLeuProTyrIleArgAlaIleValLys  360
Db      1021  GATACACTCCGTTCACCAAGTGCACCTCAAAACCTTCCTTACATTAGGCGCATTTGGAG  1080
Qy      361  GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys  380
Db      1081  GAGACATTCCTCGAATGCACCCACCTCCACAGTGCMAAAGAAATGCACAGAAAGTGT  1140
Qy      381  ***IleAsnGly***Ala***ProGluGlyAlaLeu*****PheAsnValTyrGlnVal  400
Db      1141  GAGATTAAATGGATATGTATCATCCACAGAGGAGCATTTGTCTTTCAATGTTTGGCAGAT  1200
Qy      401  Gly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu  420
Db      1201  GGAAGAGCCCAAAATACTGGGACAGACCATCAGAAATTCGTCGCCAGAGGTTCTTAGA  1260
Qy      421  Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu  440
Db      1261  ACTGCGCGCTGAAAGGGGAGAGCGGCCCTCTTGAATCTTAGGGGCGCACATTTCCAACTCC  1320
Qy      441  ProPheGlySerGlyValArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala  460
Db      1321  CCATTTCGGCTGGAGAGAGATGTGCCCTGTGATCTAGGGGCGCACATTTCCAACTCC  1380
Qy      461  ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln  480
Db      1381  ACACTTCTTCGATCTTATCATCATGCTTTGACCTGCACAGTGTGGGCGCTCAAGAGCA  1440
Qy      481  IleLeuLysGly***AspAlaLysValSerMetGluLysArgAlaGlyLeuThrValPro  500
Db      1441  AATATTGAAGGTACCAATGCCAAAGTTACACAGAAAGAGCGTGGCTCCACCGTTCCA  1500
Qy      501  ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu  520
Db      1501  AAGGACATATGTCGTGTTGTGTTCACCTTGCAGAGATGGGCGTTCATTAATCTCTT  1560
Qy      521  Ser 521
Db      1561  TCT 1563

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341 Asp\*\*\*LeuValAspGluValAspThrGlnAsnLeuProGlyTyrLeuArgAlaIleValGly 360  
Db 1087 GATGACCTCTTACGAAAGTTGAACTCAAAACCTCTTACATTAGGCGCATTTGGAAG 1146  
Qy 361 GUTRPharMechiSProProLeuProValIleValArgGlyCys\*\*\*GluGluCys 380  
Db 1147 GAGACATTCGCAATGCAACCCACCTCCAGTGTCAAAAGAAAGTGCACAGAAAGTGT 1206  
Qy 381 \*\*\*IleAsnGly\*\*\*Val\*\*\*ProGluGluAlaLeu\*\*\*PheAsnValTrpGlnVal 400  
Db 1207 GAGATTATGGAATGATATCCAGAGGAGCATTTGTTTTCATGTTTGGCAAGTA 1266  
Qy 401 Gly\*\*\*Asp\*\*\*LysTrpTrpAspArgProSerGlu\*\*\*ArgProGluArgPheLeuGlu 420  
Db 1267 GGAAAGGACCCCAATACTGGGACAGACCATCATGATTCGTCGCCAGAGGTTCTTAGAA 1326  
Qy 421 Thr\*\*\*AlaGluGluGluAla\*\*\*\*\*LeuAspLeuArgGly\*\*\*HisPheGlnLeuLeu 440  
Db 1327 ACTGCTCTGCAAGGGAAGGAGGAGGCTCTTGAATCTTAGGGGCGACATTTCCAACTCC 1386  
Qy 441 ProPheGlySerGlyArg\*\*\*MetCysProGlyVal\*\*\*LeuAlaThrSerGly\*\*\*Ala 460  
Db 1387 CCAATTGGCTCTGGAGAGATGTCCTGTGTCAATTTGGCTTACAGATGGCA 1446  
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValIleGluGlyProGlnGlyGln 480  
Db 1447 AACACTCTTCACATCTTATCCAAATGCTTGAACCTGCAAGTGTGGGCGCTCAAGAGCA 1506  
Qy 481 IleLeuArgGly\*\*\*AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500  
Db 1507 ATATTGAAGGTATGATGACCAAGTATGACATGAGAGAGAGAGCTGAGCTTCAAGTTCA 1566  
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520  
Db 1567 AGGGACATAGTCTGTTGTGTTGTTCACTTGCAGAGATGGCGTTCAATAACTCTT 1626  
Qy 521 Ser 521  
Db 1627 TCT 1629

RESULT 4  
US-09-857-581-1  
; Sequence 1. Application US/09857581  
; GENERAL INFORMATION:  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isocitrate Synthase  
; FILE REFERENCE: B01339 PCT  
; CURRENT APPLICATION NUMBER: US/09/857,581  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 60/117,769  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: 60/144,783  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/156,094  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 66

SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 1756  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-857-581-1  
Alignment Scores:  
Pred. No.: 1,51e-259 Length: 1756  
Score: 2269.00 Matches: 454  
Percent Similarity: 87.14% Conservative: 0  
Best Local Similarity: 87.14% Mismatches: 67  
Query Match: 94.70% Indels: 0  
Gaps: 0  
US-09-857-581-66 (1-521) x US-09-857-581-1 (1-1756)  
Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu\*\*\*ValLeuAlaLeuPhe\*\*\*HisLeuArgPro 20  
Db 67 ATGTGCTGGAACTTCACATTTGTTGTGTAGCTTGTGTTCTGCACTTCTGCTGCTCC 126  
Qy 21 ThrPro\*\*\*Ala\*\*\*SerLysAlaLeuArgHisLeuProAsnProSerPro\*\*\*Pro 40  
Db 127 ACACCAAGTGCAAATCAAAAGCACTTGCACCTTCCAAACCTTCCAAAGCC 186  
Qy 41 ArgLeuProPheIleGlyHis\*\*\*HisLeuLeuLysAspLysLeuLeuHisTyrAla\*\*\* 60  
Db 187 CGCTCTCTTCATTTGGCCACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 246  
Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer\*\*\*\*\*PheGlySerMetProThr 80  
Db 247 ATGATCTCTTCAAAAGCAATGGCCCTTATTTCTCTCTCTCTCTCTCTCTCTCTCT 306  
Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln\*\*\*\*\*GluAlaThrSer 100  
Db 307 GTGCTGCTTCCACCCCTGAGTGTTCAGCTTCTTCCAAACCCAGAGCAACTTCC 366  
Qy 101 Phe\*\*\*ThrArgPheGlnThrSerAla\*\*\*Arg\*\*\*LeuThrTyrAsp\*\*\*\*\*ValAla 120  
Db 367 TTCAACACAGGTTCACAAACCTCTGCAATGACCCCTCACTTACAGCAACTCTGTGGCC 426  
Qy 121 \*\*\*\*\*Pro\*\*\*GlyProTyrTrp\*\*\*PheValAlaArgLysLeuIleMetAsnAspLeuLeu 140  
Db 427 ATGCTTCATTCGACCTTACTGGAAGTTCGTGAGAAAGCTCATATGACACTTCTTC 486  
Qy 141 AsnAlaThrThrValAsn\*\*\*LeuArgProLeuArgThrGlnGlnIleArgLys\*\*\*Leu 160  
Db 487 AACGCCACACCGTCAACAGCTCAGGCTTTGAGGACCCCAAGATCCGCAAGTTCTT 546  
Qy 161 Arg\*\*\*MetAlaGln\*\*\*AlaGluAla\*\*\*LysProLeuAsp\*\*\*ThrGluGluLeuLeu 180  
Db 547 AGGCTTATGGCCCAAGGCGCAGAGGCCCAAGCCCTTCACTTCACTTCACTTCACTT 606  
Qy 181 LysTrp\*\*\*AsnSerThr\*\*\*SerMetMet\*\*\*LeuGlyGluAlaGlnIleArgAsp 200  
Db 607 AATGACCAACAGACACATCTCAATGATGATGCTGGCGAGGCTGAGAGATGAGAGAC 666



Db 247 ATGATCTCTCCAAAAGCATGCGCCCTTATCTCTCTCTCTGCGCATTCAGCAAC 306  
 QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln\*\*\*\*\*GluAlaThrSer 100  
 Db 307 GTCTGTCTCTCCACCCCTGAGTGTTCATCTCTCTCTCCAAACCCAGAGCAATCTCC 366  
 QY 101 Phe\*\*\*ThrArgPheGlnThrSerAla\*\*\*Arg\*\*\*LeuThrTyrAsp\*\*\*\*\*ValAla 120  
 Db 367 TTCACACAGAGTTCACAACTCTGCGCATAGAGCGCTCACTTACAGCACTCTGTGGCC 426  
 QY 121 \*\*\*\*\*Pro\*\*\*GlyProTyrTrp\*\*\*PheValArgLysLeuIleMetAsnAspLeuLeu 140  
 Db 427 ATGCTTCATTCGACCTTACTGAGAGTTCGTAGAGAAAGCTCATCTAGAGCACTTCTTC 486  
 QY 141 AsnAlaThrThrValAsn\*\*\*LeuArgProLeuArgThrGlnGlnIleArgLys\*\*\*Leu 160  
 Db 487 AAGCGACCAACCGTCACAAAGAGCTGAGCGCTTGGAGAACCCACAGATCCGCAATTCCTT 546  
 QY 161 Arg\*\*\*MetAlaGln\*\*\*AlaGluAla\*\*\*LysProLeuAsp\*\*\*ThrGluGluLeuLeu 180  
 Db 547 AGGGTTATGCGCCAAAGCGCAGAGCGCCAGAAAGCCCTTGATCGTCACGAGAGACTTCTC 606  
 QY 181 LysTrp\*\*\*AsnSerThr\*\*\*SerMetMet\*\*\*LeuGlyGluAlaGluGlnIleArgAsp 200  
 Db 607 AATGACACCAAGCAAGCAACATCTCCATGATGATCTGCGAGGCTTGGAGAGATCAGAGAC 666  
 QY 201 IleAlaArgGluValLeuLysIle\*\*\*GlyGluTyrSerLeuThrAspPheIle\*\*\*Pro 220  
 Db 667 ATCCCTCCGAGGTTCTTAAAGATCTTGGCGAATACAGCCCTCACTGACTCATCTGGCCT 726  
 QY 221 LeuLys\*\*\*LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240  
 Db 727 TTGAAGTATCTCAAGGTTGCAAGATGAGAAAGAGATGATGATCATCTGACAAGTTTC 786  
 QY 241 AspProValValGluArgValIleLysLysArgArg\*\*\*IleValArgArgArg\*\*\*Asn 260  
 Db 787 GACCTCTCGCTTGAAGAGGCTCATAGAGCCCGCTGAGATCGTCAGAGAGAGAAAGAAC 846  
 QY 261 GlyLys\*\*\*\*\*GluGlyGlu\*\*\*SerGlyVal\*\*\*LeuAspThrLeuLeuGluPheAla 280  
 Db 847 GAGGAAGTTGTTGAGGCGAGAGCGAGCGGCTTCTCGACACTTTCCTTGAATTCGCT 906  
 QY 281 GluAspGluThr\*\*\*GluIleLysIleThrLys\*\*\*\*\*IleLysGlyLeuValAlaAsp 300  
 Db 907 GAGGACAGACATGAGAGATCAAAATTACAGAGAGCAAAATCAAGGCGCTTGTTCGAC 966  
 QY 301 \*\*\*PheSerAlaGly\*\*\*AspSerThrAla\*\*\*\*\*ThrGluTrpAlaLeuAlaGluLeu 320  
 Db 967 TTTTCTCTCGAGGAGCATTCACAGCGGTGCGAACAGAGTGGSCATTCGCGAGCTC 1026  
 QY 321 IleAsnAspPro\*\*\*ValLeu\*\*\*\*\*AlaArgGluGlu\*\*\*TyrSerValAlaGlyLys 340  
 Db 1027 ATCAACATATCCAGGCTGTTCAAAGAGCTCTGAGAGAGTCAAGTGTGTGGCCAAA 1086  
 QY 341 Asp\*\*\*LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360

Db 1087 GATAGACTCGTTGACGAGAGTGAACACTTAACTTCTTACTTACATTTGGGCCATTTGGAG 1146  
 QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys\*\*\*GluGluCys 380  
 Db 1147 GAGACATTCGCAATGACACCCACCACTCCAGTGTGTCAAAAAGAGGACAGAGAGTGT 1206  
 QY 381 \*\*\*IleAsnLys\*\*\*Val\*\*\*ProGluGlyAlaLeu\*\*\*\*\*PheAsnValTyrGlnVal 400  
 Db 1207 GAGATTAAGGATATGATGCCAGAGAGGAGCATTTGTTCTTTTCATATGTTGGCAAGTA 1266  
 QY 401 Gly\*\*\*Asp\*\*\*LysTyrTrpAspArgProSerGlu\*\*\*ArgProGluLysArgPheLeuGlu 420  
 Db 1267 GGAAGGAGACCCCAATATCTGGACAGACATCAAGATTCCTCCAGAGGTTCTTGA 1326  
 QY 421 Thr\*\*\*AlaGluGlyGluAla\*\*\*\*\*LeuAspLeuArgGly\*\*\*HisPheGlnLeuLeu 440  
 Db 1327 ACTGTGCTGAAAGGCGAGAGAGGCGCTTGAATCTTACGGGCGCAGCATTCCAATCTCTC 1386  
 QY 441 ProPheGlySerGlyArg\*\*\*MetCysProGlyVal\*\*\*LeuAlaThrSerGly\*\*\*Ala 460  
 Db 1387 CCAATTGGGTGTGGAGAGAGATGCGCTGTGTCAATTGCTACTTACAGAAATGGCA 1446  
 QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480  
 Db 1447 ACACTTCTTGATCTCTTATCCAAATCTTTCAGCTGCAAGTCTGGGCCCTCCAGAGCAA 1506  
 QY 481 IleLeuLysGly\*\*\*AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500  
 Db 1507 ATTTCAAGAGTATGATGATGCGCAAGGTATGAGAGAGAGAGAGAGAGAGAGAGAG 1566  
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520  
 Db 1567 AGGCAACATATCTCGTTGTGTTCACCTTGCAGAGATCGGCGTTCATCTTAACTCTT 1626  
 QY 521 Ser 521  
 Db 1627 TCT 1629

RESULT 6  
 US-10-104-706A-1  
 ; Sequence 1, Application US/10104706A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Odehl, Joan  
 ; APPLICANT: Yu, Xiaodan  
 ; APPLICANT: Xu, Hu  
 ; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and Its Use  
 ; FILE REFERENCE: B81468 US NA  
 ; CURRENT APPLICATION NUMBER: US/10/104,706A  
 ; PRIORITY FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: 60/278379  
 ; PRIOR FILING DATE: March 23, 2001  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 1  
 ; LENGTH: 1756  
 ; TYPE: DNA

Alignment Scores:		
Pred. No.:	1,51e-259	Length: 1756
Score:	2269.00	Matches: 454
Percent Similarity:	87.11%	Conservative: 0
Best Local Similarity:	87.11%	Mismatches: 67
Query Match:	94.70%	Indels: 0
DB:	40	Gaps: 0

Qy	1	MettLeuLeuGluLeuLysLeuGluLeu***ValLeuAlaLeuPhe***HisLeuArgPro	20
Db	67	ATGTTGCTGCAGACTTCACCTTGCTTTGTGTGTGTACTTTGCTTCTTCGACCTGGCTGCC	120
Qy	21	ThrPro***Ala***SerLysAlaLeuArgHisLeuProAspProSerPro***Pro	40
Db	127	ACACCAAGTACCAAAATCAAAACCACTTCGGCACCTCCCAAAACCTTCACCAACCAAGCTC	180
Qy	41	ArgLeuLysProPheLysGlyHis***HisLeuLeuLysAspLysLeuLeuHisGlyTrpAla***	60
Db	187	CGCTTCCTCCCTCATGAGCCACACTTCACCTCTTAAAGATTAACCTTCCTCCATATACACTC	240
Qy	61	IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr	80
Db	247	ATCGATCTCTTCGAAAAAGATAGGCCCTTATCTCTCTCTCTCGCTGGCTTCATGCCAAC	300
Qy	81	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln****GluAlaThrSer	100
Db	307	GTCGTTCCTCCACCCCTCATGTTGTCATACGCTCTTCTCCCAAAACCCACAGAGCAACTTCC	360
Qy	101	Phe***ThrArgPheGluThrSerAla***Arg***LeuThrTrpAsp*****ValAla	120
Db	367	TTCAACACAGGTTCCAAACCTCTGCATTAAGACGCTCTACTCTACGACCAACTCTGTGGCC	420
Qy	121	****Pro***GlyProTyrTrp***PheValArgLysLeuLysLeuAspLeuLeu	140
Db	427	ATGCTTCATTCGGACCTTACTCGAAGATTCGTGTAGGAAGCTCATCATGAACACCTTCTC	480
Qy	141	AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys**Leu	160
Db	487	AACGCCACACCCGTCAACAGCTCAAGCGCTTTTAGGACCCAAACAGATCCGCAAGTTCCCT	540
Qy	161	Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLeu	180
Db	547	ACGGTTATGCGCCCAAGACGACAGAGGCCACAAACCCCTTGAACGACCAAGAGACTTCTC	600
Qy	181	LysTrp***AsnSerThr***SerMetMet***LeuGlyLysAlaGluGluIleArgAsp	200
Db	607	AAATGACCAACAGCACATCTCCATATATATCTCTGGGAGGCTGAGGAGATCCAGAAC	660
Qy	201	IleAlaArgGluValLeuLysHis***GlyGlyLysSerLeuThrAspPheIle***Pro	220
Db	667	ATCGCTGCGCAGGTTCTTAAATCTTCGGCGAAATACAGCTCTACATGACTTACCTGGCT	720

Qy	221	LeIyL***LeuYsValGIyLyTyGlyLwValaGIleAspAspIleLeuAsnIysPhe	240
Db	727	TTGAAGATCTCAAGGATGGAAAGTATGAAAGAGATATATACATCTTAAACAAGCTC	786
Qy	241	AspProValValGIuArValIleTyLysArgArg***IleValArgArg***Asn	260
Db	787	GACCTGTCGTGTAAGGATCTATCAAGACCCCTGAGATCTCGAAGCAAGAAACAC	846
Qy	261	GIyLiu*****GIuGIyGIu***SerGIyVal***LeuAspThrLeuLeuGIuPheAla	280
Db	847	GGAGAAAGTTGTGAGGGCGAGGCGAGGGGGCTTCCTCGACACTTGGCTGAATTCGCT	906
Qy	281	GIuAspGIuThr***GIuIleLysIleThrLys*****IleLysGIyLeuValAsp	300
Db	907	GAGGACGAGACATGAGATCAAAATTTACCAAGCAAGCAAAACAGGACCTTGTCGAC	966
Qy	301	***PheSerAlaGIy***AspSerThrAla*****ThrGIuThrAlaLeuAlaGIuLeu	320
Db	967	TTTTTCTCTGACAGGACAGATTCCACAGCGGTGGCAACAGAGGGCAATTGCGAGCTC	1028
Qy	321	IleAsnAspPro***ValLeu*****AlaArgGIuGIu***TyrSerValaGIyLys	340
Db	1027	ATCAACATATCCAGGGGTGTGTCCAAAGGCTCTGAGAGGATCTACAGTCTGTGGCCAA	1088
Qy	341	Asp***IleuValAspGIuValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys	360
Db	1087	GATACATCTCGTTCAGCAAGTTGACATCTCAAAACCTTCTTACATTAGGGCCATTGGAG	1146
Qy	361	GIuThrPheArgMetHisProProLeuProValValLysArgLysCys***GIuGIuCys	380
Db	1147	GAGCATTCGGAATGACCAACCACTCCACGTCGCAAAAGAAAGTGCACGAAGAGTAT	1206
Qy	381	***IleAsnGIy***Val***ProGIuGIuAlaLeu*****PheAsnValTyrGlnVal	400
Db	1207	GAGATTATGGGATATGATATATCCACAGGAGCATTTGGTCTTTTCAATGTTGGCAAGTA	1266
Qy	401	GIy***Asp***LysTyrTyrAspArgProSerGIu***ArgProGIuArgPheLeuGIu	420
Db	1267	GGAAAGGACCCCAAAATATCTGGGACAGACATCAAGATTCGTCGGAAGGTTCTTAGAA	1326
Qy	421	Thr***AlaGIuGIyGIuAla*****LeuAspLeuArgGIy***HisPheGlnLeuLeu	440
Db	1327	ACTGATGTCGTAAGGGGAGAGCGGACCTCTTGATCTTATGGGGGACAGATTTCACATCTC	1386
Qy	441	ProPheGIySerGIyArg***MetCysProGIyVal***LeuAlaThrSerGIy***Ala	460
Db	1387	CCATTTGGTGTCGGAGAGATATGTCCTCGGTGTCAATTTGGCTACTTCAGAAATGGCA	1446
Qy	461	ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGIuProGIuGIyGln	480
Db	1447	AACATCTTCGATCTCTTATCCATATGCTTAACTGACCTGCAAGTGCTGGGCCCTTCAGAGCA	1506
Qy	481	IleLeuLysGIy***AspAlaLysValaSerMetGIuLysArgAlaGIyLeuThrValPro	500
Db	1507	ATATTGAAGAGGTGATGATGCCAAAGTTAGCAGGAAGAGAGACTGGCTCAGCAAGTTCCA	1566
Qy	501	ArgAlaHisSerIleuValCysValaProLeuAlaArgIleGIyAlaIleSerLysLeuLeu	520







